

Yong Pak

#6

BIOTECHNOLOGY  
SYSTEMS  
BRANCH

**RAW SEQUENCE LISTING  
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/619,047

Source: 1652

Date Processed by STIC: 3/8/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/619,047

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2      Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3      Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4      Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5      Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6      Variable Length      Sequence(s)      contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7      PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)                     . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8      Skipped Sequences      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9      Skipped Sequences      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                         <400> sequence id number  
                         000
- 10      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11      Use of <213>Organism      Sequence(s)                      are missing this mandatory field or its response.  
(NEW RULES)
- 12      Use of <220>Feature      Sequence(s) 27 are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13      PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
"file," resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1652

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/619,047

DATE: 03/08/2001  
 TIME: 14:25:01

Input Set : A:\sequence  
 Output Set: N:\CRF3\03082001\I619047.raw

3 <110> APPLICANT: Leng, Jay  
 5 <120> TITLE OF INVENTION: PROTEASE SPECIFIC CLEAVABLE LUCIFERASES AND METHODS OF  
 6 USE THEREOF  
 8 <130> FILE REFERENCE: 105175-159907  
 10 <140> CURRENT APPLICATION NUMBER: US/09/619,047  
 11 <141> CURRENT FILING DATE: 2000-07-18  
 13 <160> NUMBER OF SEQ ID NOS: 29  
 15 <170> SOFTWARE: PatentIn Ver. 2.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 936  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Renilla reniformis  
 22 <220> FEATURE:  
 23 <221> NAME/KEY: CDS  
 24 <222> LOCATION: (1)..(936)  
 26 <400> SEQUENCE: 1  
 27 atg act tcg aaa gtt tat gat cca gaa caa agg aaa cgg atg ata act 48  
 28 Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr  
 29 1 5 10 15  
 31 ggt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt ctt gat tca 96  
 32 Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser  
 33 20 25 30  
 35 ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct gtt att 144  
 36 Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile  
 37 35 40 45  
 39 ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga cat gtt gtg 192  
 40 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val  
 41 50 55 60  
 43 cca cat att gag cca gta gcg cgg tgt att ata cca gat ctt att ggt 240  
 44 Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly  
 45 65 70 75 80  
 47 atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta ctt gat 288  
 48 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp  
 49 85 90 95  
 51 cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta cca aag 336  
 52 His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys  
 53 100 105 110  
 55 aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca ttt cat 384  
 56 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His  
 57 115 120 125  
 59 tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac gct gaa 432  
 60 Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu  
 61 130 135 140  
 63 agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat att gaa 480  
 64 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu  
 65 145 150 155 160  
 67 gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa atg gtt ttg 528

Does Not Comply  
 Corrected Diskette Needed

P. 6

RAW SEQUENCE LISTING                      DATE: 03/08/2001  
 PATENT APPLICATION: US/09/619,047        TIME: 14:25:01

Input Set : A:\sequence  
 Output Set: N:\CRF3\03082001\I619047.raw

```

68 Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
69          165          170          175
71 gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa atc atg aga 576
72 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
73          180          185          190
75 aag tta gaa cca gaa gaa ttt gca gca tat ctt gaa cca ttc aaa gag 624
76 Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
77          195          200          205
79 aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt gaa atc ccg 672
80 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
81          210          215          220
83 tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt agg aat tat 720
84 Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
85 225          230          235          240
87 aat gct tat cta cgt gca agt gat gat tta cca aaa atg ttt att gaa 768
88 Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
89          245          250          255
91 tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc gcc aag aag 816
92 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
93          260          265          270
95 ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat ttt tcg caa 864
96 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
97          275          280          285
99 gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg ttc gtt gag 912
100 Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
101          290          295          300
103 cga gtt ctc aaa aat gaa caa taa 936
104 Arg Val Leu Lys Asn Glu Gln
105 305          310
108 <210> SEQ ID NO: 2
109 <211> LENGTH: 311
110 <212> TYPE: PRT
111 <213> ORGANISM: Renilla reniformis
113 <400> SEQUENCE: 2
114 Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
115 1 5 10 15
116 Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
117 20 25 30
118 Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
119 35 40 45
120 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
121 50 55 60
122 Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
123 65 70 75 80
124 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
125 85 90 95
126 His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
127 100 105 110
128 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His

```

## RAW SEQUENCE LISTING

DATE: 03/08/2001

PATENT APPLICATION: US/09/619,047

TIME: 14:25:01

Input Set : A:\sequence

Output Set: N:\CRF3\03082001\I619047.raw

```

129          115          120          125
130 Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
131          130          135          140
132 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
133 145          150          155          160
134 Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
135          165          170          175
136 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
137          180          185          190
138 Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
139          195          200          205
140 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
141          210          215          220
142 Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
143 225          230          235          240
144 Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
145          245          250          255
146 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
147          260          265          270
148 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
149          275          280          285
150 Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
151          290          295          300
152 Arg Val Leu Lys Asn Glu Gln
153 305          310
157 <210> SEQ ID NO: 3
158 <211> LENGTH: 936
159 <212> TYPE: DNA
160 <213> ORGANISM: Renilla reniformis (mutated sequence)
162 <220> FEATURE:
163 <221> NAME/KEY: CDS
164 <222> LOCATION: (1)..(936)
166 <400> SEQUENCE: 3
167 atg act tcg aaa gtt tat gat cca gaa caa agg aaa cgg atg ata act 48
168 Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
169 1 5 10 15
171 ggt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt ctt gat tca 96
172 Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser.
173 20 25 30
175 ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct gtt att 144
176 Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
177 35 40 45
179 ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga cat gtt gtg 192
180 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
181 50 55 60
183 cca cat att gag cca gta gcg cgg tgt att ata cca gat ctt att ggt 240
184 Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
185 65 70 75 80
187 atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta ctt gat 288

```

## RAW SEQUENCE LISTING

DATE: 03/08/2001

PATENT APPLICATION: US/09/619,047

TIME: 14:25:01

Input Set : A:\sequence

Output Set: N:\CRF3\03082001\I619047.raw

```

188 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
189           85           90           95
191 cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta cca aag 336
192 His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
193           100           105           110
195 aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca ttt cat 384
196 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
197           115           120           125
199 tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac gct gaa 432
200 Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
201           130           135           140
203 agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat att gaa 480
204 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
205 145           150           155           160
207 gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa atg gtt ttg 528
208 Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
209           165           170           175
211 gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa atc atg aga 576
212 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
213           180           185           190
215 aag tta gaa cca gac gaa gtt gac gca tat ctt gaa cca ttc aaa gag 624
216 Lys Leu Glu Glu Pro Asp Glu Val Asp Ala Tyr Leu Glu Pro Phe Lys Glu
217           195           200           205
219 aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt gaa atc ccg 672
220 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
221           210           215           220
223 tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt agg aat tat 720
224 Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
225 225           230           235           240
227 aat gct tat cta cgt gca agt gat gat tta cca aaa atg ttt att gaa 768
228 Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
229           245           250           255
231 tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc gcc aag aag 816
232 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
233           260           265           270
235 ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat ttt tcg caa 864
236 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
237           275           280           285
239 gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg ttc gtt gag 912
240 Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
241           290           295           300
243 cga gtt ctc aaa aat gaa caa taa 936
244 Arg Val Leu Lys Asn Glu Gln
245 305           310
248 <210> SEQ ID NO: 4
249 <211> LENGTH: 311
250 <212> TYPE: PRT
251 <213> ORGANISM: Renilla reniformis (mutated sequence)
253 <400> SEQUENCE: 4

```

## RAW SEQUENCE LISTING

DATE: 03/08/2001

PATENT APPLICATION: US/09/619,047.

TIME: 14:25:01

Input Set : A:\sequence

Output Set: N:\CRF3\03082001\I619047.raw

```

254 Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
255   1           5           10           15
256 Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
257           20           25           30
258 Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
259           35           40           45
260 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
261           50           55           60
262 Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
263   65           70           75           80
264 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
265           85           90           95
266 His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
267           100          105          110
268 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
269           115          120          125
270 Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
271           130          135          140
272 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
273 145          150          155          160
274 Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
275           165          170          175
276 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
277           180          185          190
278 Lys Leu Glu Pro Asp Glu Val Asp Ala Tyr Leu Glu Pro Phe Lys Glu
279           195          200          205
280 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
281           210          215          220
282 Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
283 225          230          235          240
284 Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
285           245          250          255
286 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
287           260          265          270
288 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
289           275          280          285
290 Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
291           290          295          300
292 Arg Val Leu Lys Asn Glu Gln
293 305          310
297 <210> SEQ ID NO: 5
298 <211> LENGTH: 8
299 <212> TYPE: PRT
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Description of Artificial Sequence: Protease
304      recognition sequences
306 <400> SEQUENCE: 5
307 Ser Gln Asn Tyr Pro Ile Val Gln

```

09/6/9,047 6

<210> 27

<211> 8

<212> PRT

<213> Artificial Sequence

*see item 12 on Env Summary Sheet*

<400> 27

Arg Pro Leu Gly Ile Ile Gly Gly

1

5

FYI

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/619,047

DATE: 03/08/2001

TIME: 14:25:02

Input Set : A:\sequence

Output Set: N:\CRF3\03082001\I619047.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
 L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:551 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22  
 L:551 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22  
 L:551 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22  
 L:568 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23  
 L:568 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23  
 L:568 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23  
 L:613 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26  
 L:613 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
 L:613 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26  
 L:622 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:622 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: